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Dispersal processes underlying the recent pandemic caused by the plant pathogenic fungus *Mycosphaerella fijiensis*

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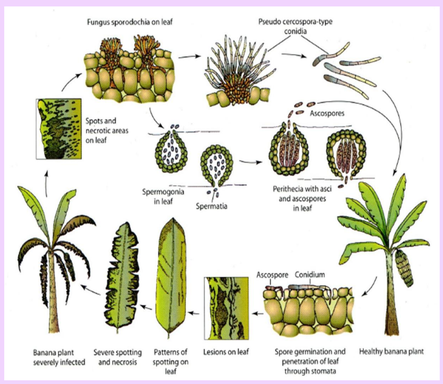
▪ CONTEXT & OBJECTIVES

How plant pathogenic fungi spread is the first question to consider for understanding the emergence of diseases caused by such organisms.

The ascomycete fungus *Mycosphaerella fijiensis,* causing the black leaf streak disease of banana, is an example of a recent pandemic in agriculture and a good model to address this question in the case of an aerial plant pathogen. The pandemic started around 1960 from the South-East Asia and *M. fijiensis* has spread to almost all banana producing areas for the last 40 years.



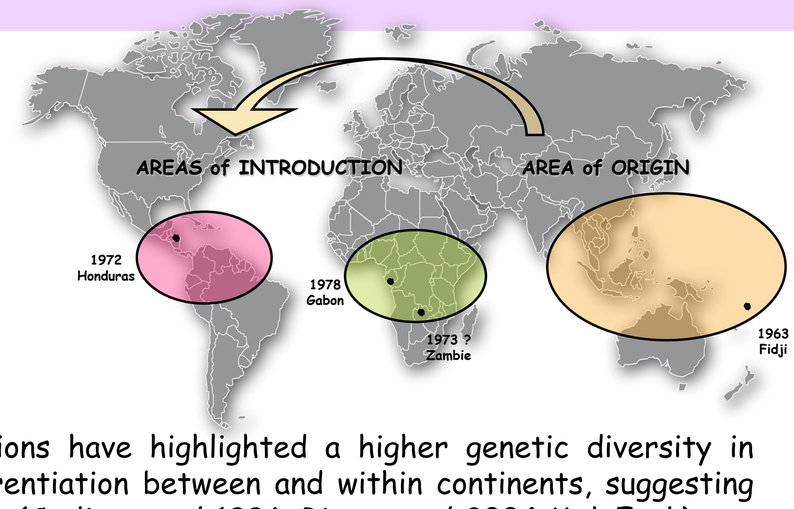
Life cycle of *Mycosphaerella fijiensis*
From Agrios, George N. 2005.

Dispersal modes of *M. fijiensis*:

- Infected plant material
- Ascospores (sexual cycle)
- Conidia (asexual cycle)

A convenient biological model for population genetics and phylogeographic studies:

- Existence of sexual reproduction
- Stable and panmictic populations
- Historical data about global spread available



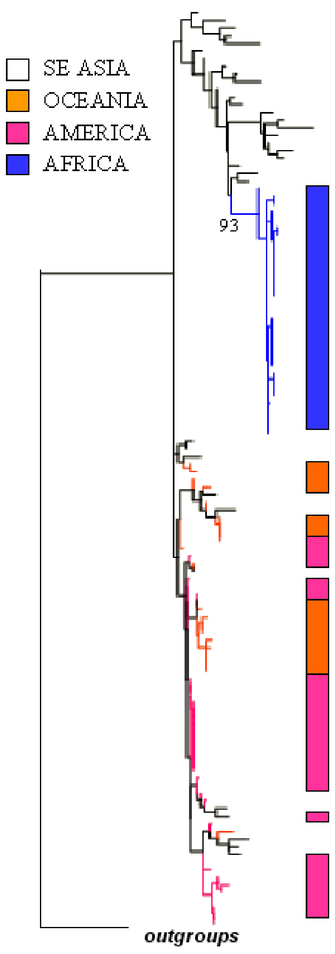
Previous studies of genetic structure of populations have highlighted a higher genetic diversity in South-East Asia, and high levels of genetic differentiation between and within continents, suggesting that founder events have accompanied the pandemic (Carlier *et al*, 1996; Rivas *et al*, 2004 Mol. Ecol.).

A further investigation of the dispersal processes underlying the pandemic is now required.

Objectives:

- **To infer historical and demographic events (bottlenecks, admixture) undergone by invading populations**
- **To reconstruct global routes of dissemination and clarify dispersal modes of the pathogen**

▪ PHYLOGEOGRAPHY STUDY AT GLOBAL SCALE

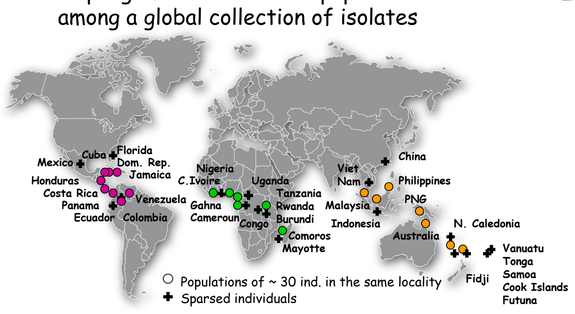


✓ Molecular phylogenetic analysis

120 *M. fijiensis* individuals
8 sequence-based nuclear markers

Phylogenetic tree reconstructed by the maximum likelihood method

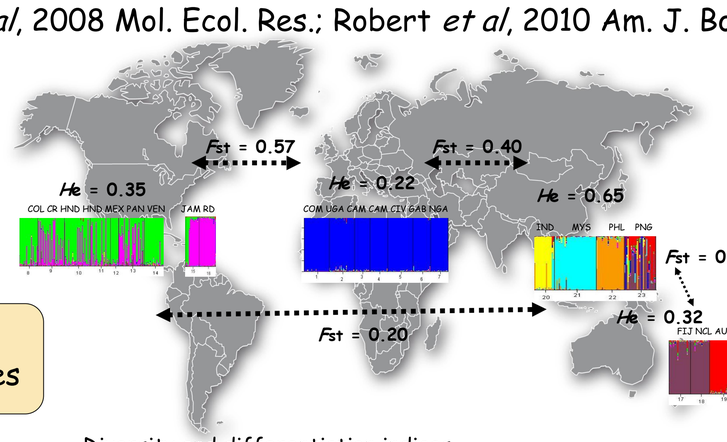
Sampling of individuals and populations among a global collection of isolates



Low level of intraspecific polymorphism
Markers of old events of introductions

✓ Explorative population genetics analysis

23 populations (~700 individuals)
21 microsatellite markers
(Zapater *et al*, 2008 Mol. Ecol. Res.; Robert *et al*, 2010 Am. J. Bot.)

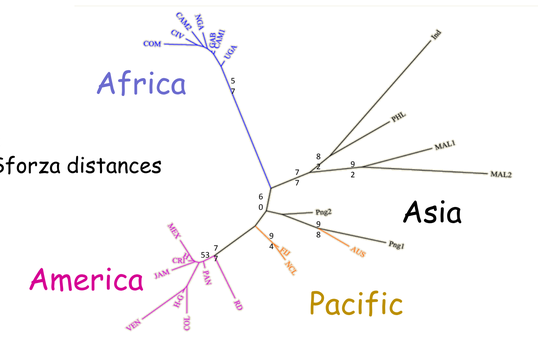


High level of polymorphism
Markers of fine-scale dispersal processes

Diversity and differentiation indices,
Clustering analysis (STRUCTURE)

These different analysis were congruent and suggested strong hypotheses:

- **An only successful introduction in AFRICA, probably associated with a bottleneck, explaining emergence of an homogeneous group comparatively to the other continents**
- **A pattern of genetic admixture in AMERICA, possibly due to multiple introductions**
- **Asian origins for all these introduction events certainly from transport of infected plant materials**



✓ Perspective: test different scenarii and estimate parameters using ABC (Approximate Bayesian Computation) method

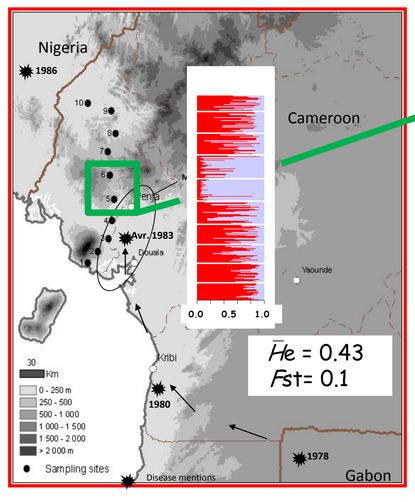
▪ SPATIAL GENETIC ANALYSIS AT LOCAL SCALE

The Cameroon situation, an example of a recently (~ 1980) colonized area

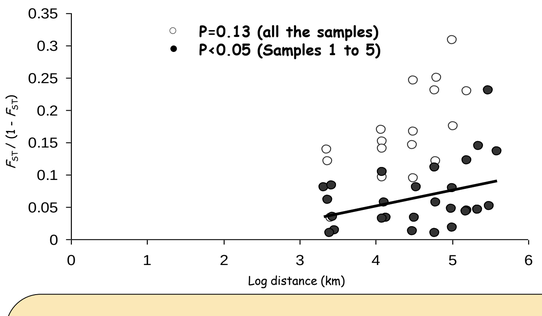
✓ Along a 300-km-long transect

(Halkett *et al*, 2010 Mol. Ecol.)

10 Populations (~ 290 individuals)
19 microsatellite markers



Diversity and differentiation indices,
Clustering analysis (STRUCTURE)



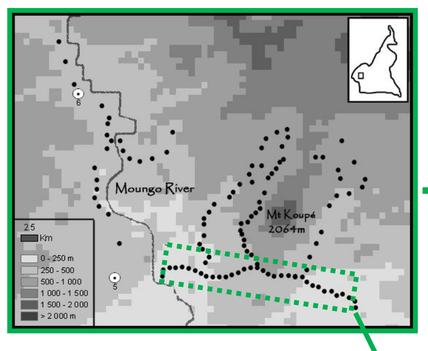
Isolation by distance analysis (discrete populations)

-A genetic discontinuity was detected at the middle of the transect (between sites 5 and 6)

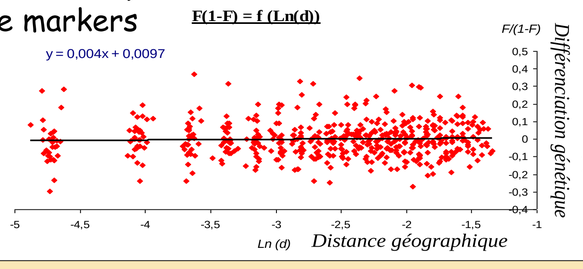
- An Isolation by distance was detected before the above discontinuity suggesting gradual dispersal through ascospores

✓ On a 50x50 km area

(Rieux *et al*, 2011 Mol. Ecol.)

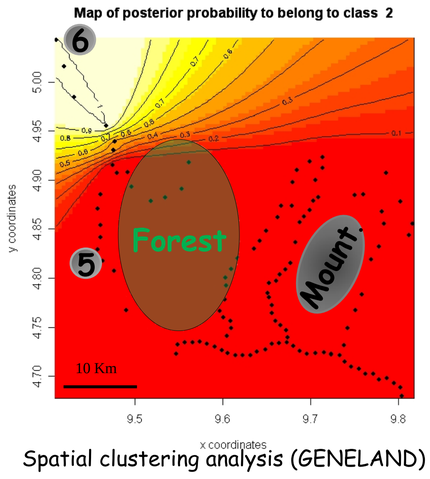


1D sampling on a 30-km-long transect
(90 sites, 321 individuals)
17 microsatellite markers



Isolation by distance analysis
(continuous populations)

2D sampling (105 sites, 570 individuals)
17 microsatellite markers



Spatial clustering analysis (GENELAND)

- The genetic discontinuity was sharp delimiting 2 populations. No landscape features matched this discontinuity ⇒ colonization trace (e.g. through gene surfing)

- No isolation by distance ⇒ high effective population size in *M. fijiensis* is suspected

✓ Perspective: estimate dispersal from allelic clines detected between the 2 populations